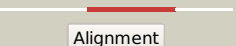
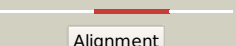
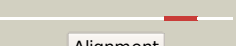


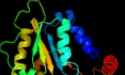
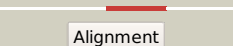

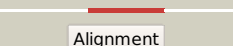

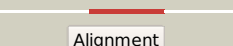

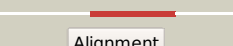

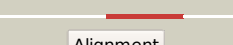

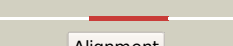







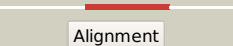
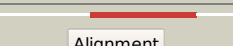


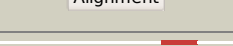
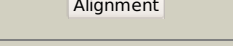
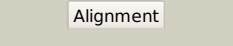
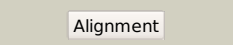
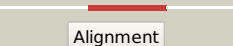


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1582c_(-)_1784504_1785919
Date	Fri Aug 2 13:30:17 BST 2019
Unique Job ID	9e6be58d1a58882b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1u0ja_	 Alignment		99.8	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
2	c2gxaA_	 Alignment		99.6	14	PDB header: replication/dna Chain: A; PDB Molecule: replication protein e1; PDBTitle: crystal structure of papillomavirus e1 hexameric helicase2 with ssdna and mgadp
3	c2v9pH_	 Alignment		99.5	18	PDB header: hydrolase Chain: H; PDB Molecule: replication protein e1; PDBTitle: crystal structure of papillomavirus e1 hexameric helicase2 dna-free form
4	d1tuea_	 Alignment		99.3	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
5	d1svma_	 Alignment		98.6	11	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
6	c4gdff_	 Alignment		98.4	11	PDB header: hydrolase/dna Chain: F; PDB Molecule: large t antigen; PDBTitle: a crystal structure of sv40 large t antigen
7	d1dp7p_	 Alignment		98.4	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: P4 origin-binding domain-like
8	c4ypnA_	 Alignment		98.3	15	PDB header: hydrolase Chain: A; PDB Molecule: lon protease; PDBTitle: crystal structure of a lona fragment containing the 3-helix bundle and2 the aaa-alpha/beta domain
9	d1ixsb2	 Alignment		98.0	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
10	c2qz4A_	 Alignment		98.0	17	PDB header: hydrolase Chain: A; PDB Molecule: paraplegin; PDBTitle: human paraplegin, aaa domain in complex with adp
11	c3u5zM_	 Alignment		98.0	10	PDB header: dna binding protein/dna Chain: M; PDB Molecule: dna polymerase accessory protein 44; PDBTitle: structure of t4 bacteriophage clamp loader bound to the t4 clamp,2 primer-template dna, and atp analog

12	c3pvsA_	 Alignment		98.0	19	PDB header: recombination Chain: A; PDB Molecule: replication-associated recombination protein a; PDBTitle: structure and biochemical activities of escherichia coli mgsa
13	c3nbxX_	 Alignment		97.9	14	PDB header: hydrolase Chain: X; PDB Molecule: atpase rava; PDBTitle: crystal structure of e. coli rava (regulatory atpase variant a) in2 complex with adp
14	c3vfdA_	 Alignment		97.9	12	PDB header: hydrolase Chain: A; PDB Molecule: spastin; PDBTitle: human spastin aaa domain
15	c6blbA_	 Alignment		97.9	11	PDB header: hydrolase Chain: A; PDB Molecule: holliday junction atp-dependent dna helicase ruvb; PDBTitle: 1.88 angstrom resolution crystal structure holliday junction atp-2 dependent dna helicase (ruvb) from pseudomonas aeruginosa in complex3 with adp
16	c5c3cB_	 Alignment		97.9	16	PDB header: protein binding Chain: B; PDB Molecule: cbbq/nirq/norq domain protein; PDBTitle: structural characterization of a newly identified component of alpha-2 carboxysomes: the aaa+ domain protein cso-cbbq
17	c3b9pA_	 Alignment		97.8	12	PDB header: hydrolase Chain: A; PDB Molecule: cg5977-pa, isoform a; PDBTitle: spastin
18	c1sxaA_	 Alignment		97.8	13	PDB header: replication Chain: A; PDB Molecule: activator 1 95 kda subunit; PDBTitle: crystal structure of the eukaryotic clamp loader (replication factor2 c, rfc) bound to the dna sliding clamp (proliferating cell nuclear3 antigen, pcna)
19	c5grbF_	 Alignment		97.8	14	PDB header: hydrolase/inhibitor Chain: F; PDB Molecule: ev71 2c atpase; PDBTitle: crystal structure of 2c helicase from enterovirus 71 (ev71) bound with2 atpgammas
20	c6nyyC_	 Alignment		97.7	19	PDB header: translocase Chain: C; PDB Molecule: afg3-like protein 2; PDBTitle: human m-aaa protease afg3l2, substrate-bound
21	d1ofha_	 Alignment	not modelled	97.7	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
22	c1r6bX_	 Alignment	not modelled	97.7	16	PDB header: hydrolase Chain: X; PDB Molecule: clpa protein; PDBTitle: high resolution crystal structure of clpa
23	c5kzfJ_	 Alignment	not modelled	97.7	16	PDB header: hydrolase Chain: J; PDB Molecule: proteasome-associated atpase; PDBTitle: crystal structure of near full-length hexameric mycobacterium2 tuberculosis proteasomal atpase mpa in apo form
24	d1sxa2	 Alignment	not modelled	97.7	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
25	d1ka8a_	 Alignment	not modelled	97.7	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: P4 origin-binding domain-like
26	c4b4tM_	 Alignment	not modelled	97.7	13	PDB header: hydrolase Chain: M; PDB Molecule: 26s protease regulatory subunit 6a; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
27	c4l16A_	 Alignment	not modelled	97.7	13	PDB header: hydrolase Chain: A; PDB Molecule: fidgetin-like protein 1; PDBTitle: crystal structure of figl-1 aaa domain in complex with adp
28	c3pxiB_	 Alignment	not modelled	97.6	14	PDB header: protein binding Chain: B; PDB Molecule: negative regulator of genetic competence clpc/mecb; PDBTitle: structure of meca108:clpc
29	c3d8bB_	 Alignment	not modelled	97.6	16	PDB header: hydrolase Chain: B; PDB Molecule: fidgetin-like protein 1;

29	c3g6vb	Alignment	not modelled	97.6	10	PDBTitle: crystal structure of human fidgetin-like protein 1 in complex with adp
30	c2chgB	Alignment	not modelled	97.6	15	PDB header: dna-binding protein Chain: B; PDB Molecule: replication factor c small subunit; PDBTitle: replication factor c domains 1 and 2
31	c4lcbA	Alignment	not modelled	97.6	14	PDB header: protein transport Chain: A; PDB Molecule: cell division protein cdvc, vps4; PDBTitle: structure of vps4 homolog from acidianus hospitalis
32	d2ce7a2	Alignment	not modelled	97.6	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
33	d1r6bx3	Alignment	not modelled	97.6	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
34	c5g4gF	Alignment	not modelled	97.6	17	PDB header: hydrolase Chain: F; PDB Molecule: vcp-like atpase; PDBTitle: structure of the atpgs-bound vat complex
35	c3eihB	Alignment	not modelled	97.6	13	PDB header: protein transport Chain: B; PDB Molecule: vacuolar protein sorting-associated protein 4; PDBTitle: crystal structure of s.cerevisiae vps4 in the presence of atpgammas
36	c6azyA	Alignment	not modelled	97.6	14	PDB header: chaperone Chain: A; PDB Molecule: heat shock protein hsp104; PDBTitle: crystal structure of hsp104 r328m/r757m mutant from calcarisporiella2 thermophila
37	c5j1sA	Alignment	not modelled	97.6	12	PDB header: hydrolase Chain: A; PDB Molecule: torsin-1a; PDBTitle: torsina-lull1 complex, h. sapiens, bound to vhh-bs2
38	c2ce7B	Alignment	not modelled	97.6	10	PDB header: cell division protein Chain: B; PDB Molecule: cell division protein ftsh; PDBTitle: edta treated
39	c6az0A	Alignment	not modelled	97.5	12	PDB header: hydrolase Chain: A; PDB Molecule: mitochondrial inner membrane i-aaa protease supercomplex PDBTitle: mitochondrial atpase protease yme1
40	c5h7i7	Alignment	not modelled	97.5	17	PDB header: hydrolase Chain: 7; PDB Molecule: dna replication licensing factor mcm7; PDBTitle: cryo-em structure of the cdt1-mcm2-7 complex in amppnp state
41	d1lqpa2	Alignment	not modelled	97.5	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
42	c1qvrB	Alignment	not modelled	97.5	14	PDB header: chaperone Chain: B; PDB Molecule: clpb protein; PDBTitle: crystal structure analysis of clpb
43	c6nyyA	Alignment	not modelled	97.5	17	PDB header: translocase Chain: A; PDB Molecule: afg3-like protein 2; PDBTitle: human m-aaa protease afg3l2, substrate-bound
44	c5z3qD	Alignment	not modelled	97.5	14	PDB header: viral protein Chain: D; PDB Molecule: pv-2c; PDBTitle: crystal structure of a soluble fragment of poliovirus 2c atpase (2.552 angstrom)
45	c2r65A	Alignment	not modelled	97.5	14	PDB header: hydrolase Chain: A; PDB Molecule: cell division protease ftsh homolog; PDBTitle: crystal structure of helicobacter pylori atp dependent protease, ftsh2 adp complex
46	d1e32a2	Alignment	not modelled	97.5	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
47	c3pfiB	Alignment	not modelled	97.5	13	PDB header: hydrolase Chain: B; PDB Molecule: holliday junction atp-dependent dna helicase ruvb; PDBTitle: 2.7 angstrom resolution crystal structure of a probable holliday2 junction dna helicase (ruvb) from campylobacter jejuni subsp. jejuni3 nctc 11168 in complex with adenosine-5'-diphosphate
48	d1in4a2	Alignment	not modelled	97.4	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
49	c5dggA	Alignment	not modelled	97.4	9	PDB header: replication Chain: A; PDB Molecule: active helicase; PDBTitle: sccmec type iv cch - active helicase
50	d1qvra3	Alignment	not modelled	97.4	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
51	c2p65A	Alignment	not modelled	97.4	14	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: hypothetical protein pf08_0063; PDBTitle: crystal structure of the first nucleotide binding domain of2 chaperone clpb1, putative, (pv089580) from plasmodium vivax
52	c5d4wB	Alignment	not modelled	97.4	17	PDB header: chaperone Chain: B; PDB Molecule: putative heat shock protein; PDBTitle: crystal structure of hsp104
53	c5vq9D	Alignment	not modelled	97.3	15	PDB header: protein binding Chain: D; PDB Molecule: pacchytene checkpoint protein 2 homolog; PDBTitle: structure of human trip13, apo form
54	c2r44A	Alignment	not modelled	97.3	11	PDB header: hydrolase Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative atpase (chu_0153) from cytophaga2 hutchinsonii atcc 33406 at 2.00 a resolution
55	c3cf2B	Alignment	not modelled	97.3	16	PDB header: transport protein Chain: B; PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97/vcp in complex with adp/amp-pnp

56	c4r7zB	Alignment	not modelled	97.3	14	PDB header: hydrolase Chain: B; PDB Molecule: cell division control protein 21; PDBTitle: pfmc-m-aaa double-octamer
57	c1hqcB	Alignment	not modelled	97.3	13	PDB header: hydrolase Chain: B; PDB Molecule: ruvb; PDBTitle: structure of ruvb from thermus thermophilus hb8
58	c4b4tL	Alignment	not modelled	97.3	10	PDB header: hydrolase Chain: L; PDB Molecule: 26s protease subunit rpt4; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
59	c6i26A	Alignment	not modelled	97.3	14	PDB header: motor protein Chain: A; PDB Molecule: midasin,midasin,midasin,midasin; PDBTitle: rea1 wild type amppnp state
60	c3jc72	Alignment	not modelled	97.3	15	PDB header: hydrolase Chain: 2; PDB Molecule: dna replication licensing factor mcm2; PDBTitle: structure of the eukaryotic replicative cmg helicase and pumpjack2 motion
61	c1in8A	Alignment	not modelled	97.2	12	PDB header: dna binding protein Chain: A; PDB Molecule: holliday junction dna helicase ruvb; PDBTitle: thermotoga maritima ruvb t158v
62	c4xgcA	Alignment	not modelled	97.2	11	PDB header: dna binding protein Chain: A; PDB Molecule: origin recognition complex subunit 1; PDBTitle: crystal structure of the eukaryotic origin recognition complex
63	c4b4tI	Alignment	not modelled	97.2	12	PDB header: hydrolase Chain: I; PDB Molecule: 26s protease regulatory subunit 4 homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
64	c4xguB	Alignment	not modelled	97.2	15	PDB header: atp-binding protein Chain: B; PDB Molecule: putative pachytene checkpoint protein 2; PDBTitle: structure of c. elegans pch-2
65	c3bosA	Alignment	not modelled	97.2	8	PDB header: hydrolase regulator,dna binding protein Chain: A; PDB Molecule: putative dna replication factor; PDBTitle: crystal structure of a putative dna replication regulator hda2 (sama_1916) from shewanella amazonensis sb2b at 1.75 a resolution
66	c6edoA	Alignment	not modelled	97.2	14	PDB header: motor protein Chain: A; PDB Molecule: midasin; PDBTitle: full-length s. pombe mdn1 in the presence of amppnp (ring region)
67	c5uj7B	Alignment	not modelled	97.2	16	PDB header: dna binding protein Chain: B; PDB Molecule: origin recognition complex subunit 1; PDBTitle: structure of the active form of human origin recognition complex2 atpase motor module, complex subunits 1, 4, 5
68	d1gvnb	Alignment	not modelled	97.2	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Plasmid maintenance system epsilon/zeta, toxin zeta subunit
69	c5ifwB	Alignment	not modelled	97.2	16	PDB header: signaling protein Chain: B; PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: quantitative interaction mapping reveals an extended ubiquitin2 regulatory domain in aspl that disrupts functional p97 hexamers and3 induces cell death
70	c3jc76	Alignment	not modelled	97.1	16	PDB header: hydrolase Chain: 6; PDB Molecule: dna replication licensing factor mcm6; PDBTitle: structure of the eukaryotic replicative cmg helicase and pumpjack2 motion
71	c5u8s4	Alignment	not modelled	97.1	14	PDB header: replication Chain: 4; PDB Molecule: dna replication licensing factor mcm4; PDBTitle: structure of eukaryotic cmg helicase at a replication fork
72	c2zamA	Alignment	not modelled	97.1	16	PDB header: protein transport Chain: A; PDB Molecule: vacuolar protein sorting-associating protein 4b; PDBTitle: crystal structure of mouse skd1/vps4b apo-form
73	d1jbka	Alignment	not modelled	97.1	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
74	c3ja83	Alignment	not modelled	97.1	14	PDB header: hydrolase Chain: 3; PDB Molecule: minichromosome maintenance 3; PDBTitle: cryo-em structure of the mcm2-7 double hexamer
75	c3ja82	Alignment	not modelled	97.1	16	PDB header: hydrolase Chain: 2; PDB Molecule: minichromosome maintenance 2; PDBTitle: cryo-em structure of the mcm2-7 double hexamer
76	d1ixza	Alignment	not modelled	97.1	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
77	c2p5tD	Alignment	not modelled	97.1	15	PDB header: transcription regulator Chain: D; PDB Molecule: pez2; PDBTitle: molecular and structural characterization of the pezat chromosomal2 toxin-antitoxin system of the human pathogen streptococcus pneumoniae
78	c1xwiA	Alignment	not modelled	97.1	16	PDB header: protein transport Chain: A; PDB Molecule: skd1 protein; PDBTitle: crystal structure of vps4b
79	c1sxjB	Alignment	not modelled	97.0	15	PDB header: replication Chain: B; PDB Molecule: activator 1 37 kda subunit; PDBTitle: crystal structure of the eukaryotic clamp loader (replication factor2 c, rfc) bound to the dna sliding clamp (proliferating cell nuclear3 antigen, pcna)
80	c3jc57	Alignment	not modelled	97.0	20	PDB header: hydrolase Chain: 7; PDB Molecule: dna replication licensing factor mcm7; PDBTitle: structure of the eukaryotic replicative cmg helicase and pumpjack2 motion
81	c5udb7	Alignment	not modelled	97.0	18	PDB header: replication Chain: 7; PDB Molecule: dna replication licensing factor mcm7; PDBTitle: structural basis of mcm2-7 replicative helicase loading by

						orc-cdc62 and cdt1
82	c1sxC_	Alignment	not modelled	97.0	16	PDB header: replication Chain: C; PDB Molecule: activator 1 40 kda subunit; PDBTitle: crystal structure of the eukaryotic clamp loader (replication factor2 c, rfc) bound to the dna sliding clamp (proliferating cell nuclear3 antigen, pcna)
83	c3cf1C_	Alignment	not modelled	97.0	17	PDB header: transport protein Chain: C; PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97/vcp in complex with adp/adp.afx
84	c6orbA_	Alignment	not modelled	97.0	15	PDB header: motor protein Chain: A; PDB Molecule: midasin; PDBTitle: full-length s. pombe mdn1 in the presence of atp and rbin-1
85	c2chvE_	Alignment	not modelled	97.0	16	PDB header: dna-binding protein Chain: E; PDB Molecule: replication factor c small subunit; PDBTitle: replication factor c adpnp complex
86	c3ja84_	Alignment	not modelled	97.0	17	PDB header: hydrolase Chain: 4; PDB Molecule: minichromosome maintenance 4; PDBTitle: cryo-em structure of the mcm2-7 double hexamer
87	c1sxE_	Alignment	not modelled	97.0	12	PDB header: replication Chain: E; PDB Molecule: activator 1 40 kda subunit; PDBTitle: crystal structure of the eukaryotic clamp loader (replication factor2 c, rfc) bound to the dna sliding clamp (proliferating cell nuclear3 antigen, pcna)
88	c4d2qC_	Alignment	not modelled	96.9	15	PDB header: chaperone Chain: C; PDB Molecule: clpb; PDBTitle: negative-stain electron microscopy of e. coli clpb mutant e432a (bap2 form bound to clpb)
89	c2x8aA_	Alignment	not modelled	96.9	14	PDB header: nuclear protein Chain: A; PDB Molecule: nuclear valosin-containing protein-like; PDBTitle: human nuclear valosin containing protein like (nvl), c-2 terminal aaa-atpase domain
90	c6djuA_	Alignment	not modelled	96.9	13	PDB header: chaperone Chain: A; PDB Molecule: chaperone protein clpb; PDBTitle: mtb clpb in complex with atpgammas and casein, conformer 1
91	c3jc73_	Alignment	not modelled	96.9	14	PDB header: hydrolase Chain: 3; PDB Molecule: dna replication licensing factor mcm3; PDBTitle: structure of the eukaryotic replicative cmg helicase and pumpjack2 motion
92	c5e7pA_	Alignment	not modelled	96.9	15	PDB header: hydrolase Chain: A; PDB Molecule: cell division control protein cdc48; PDBTitle: crystal structure of msmeq_0858 (uniprot a0qqs4), a aaa atpase.
93	c6epcJ_	Alignment	not modelled	96.9	8	PDB header: hydrolase Chain: J; PDB Molecule: 26s proteasome regulatory subunit 8; PDBTitle: ground state 26s proteasome (gs2)
94	c3zw6B_	Alignment	not modelled	96.8	8	PDB header: photosynthesis Chain: B; PDB Molecule: ribulose bisphosphate carboxylase/oxygenase activase 1, PDBTitle: model of hexameric aaa domain arrangement of green-type rubisco2 activase from tobacco.
95	c6hv93_	Alignment	not modelled	96.8	13	PDB header: dna binding protein Chain: 3; PDB Molecule: dna replication licensing factor mcm3; PDBTitle: s. cerevisiae cmg-pol epsilon-dna
96	c6i27A_	Alignment	not modelled	96.8	14	PDB header: motor protein Chain: A; PDB Molecule: midasin, midasin, midasin, midasin, midasin, midasin; PDBTitle: rea1 aaa2l-h2alpha deletion mutant in amppnp state
97	c5w0tA_	Alignment	not modelled	96.8	10	PDB header: hydrolase Chain: A; PDB Molecule: protein msp1; PDBTitle: crystal structure of monomeric msp1 from s. cerevisiae
98	c6epdM_	Alignment	not modelled	96.8	5	PDB header: hydrolase Chain: M; PDB Molecule: 26s proteasome regulatory subunit 6a; PDBTitle: substrate processing state 26s proteasome (sps1)
99	c3ja87_	Alignment	not modelled	96.8	18	PDB header: hydrolase Chain: 7; PDB Molecule: minichromosome maintenance 7; PDBTitle: cryo-em structure of the mcm2-7 double hexamer
100	c6b5cA_	Alignment	not modelled	96.8	10	PDB header: cell cycle Chain: A; PDB Molecule: katanin p60 atpase-containing subunit a-like 1; PDBTitle: structural basis for katanin self-assembly
101	c6e111_	Alignment	not modelled	96.8	15	PDB header: protein transport Chain: 1; PDB Molecule: heat shock protein 101; PDBTitle: ptex core complex in the resetting (compact) state
102	c3hteC_	Alignment	not modelled	96.8	13	PDB header: motor protein Chain: C; PDB Molecule: atp-dependent clp protease atp-binding subunit clpx; PDBTitle: crystal structure of nucleotide-free hexameric clpx
103	c4z8xC_	Alignment	not modelled	96.8	15	PDB header: hydrolase Chain: C; PDB Molecule: atp-dependent zinc metalloprotease ftsh; PDBTitle: truncated ftsh from a. aeolicus
104	c3j96F_	Alignment	not modelled	96.7	15	PDB header: hydrolase Chain: F; PDB Molecule: vesicle-fusing atpase; PDBTitle: structure of 20s supercomplex determined by single particle2 cryoelectron microscopy (state i)
105	c4b4tK_	Alignment	not modelled	96.7	13	PDB header: hydrolase Chain: K; PDB Molecule: 26s protease regulatory subunit 6b homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
106	c6on2A_	Alignment	not modelled	96.7	15	PDB header: hydrolase Chain: A; PDB Molecule: atp-dependent protease la; PDBTitle: lon protease from yersinia pestis with y2853 substrate
107	c5wc0D_	Alianment	not modelled	96.7	12	PDB header: motor protein Chain: D; PDB Molecule: meiotic spindle formation protein mei-1;

						PDBTitle: katanin hexamer in spiral conformation
108	c4b4tj_	Alignment	not modelled	96.7	9	PDB header: hydrolase Chain: J: PDB Molecule: 26s protease regulatory subunit 8 homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
109	c1nsfA_	Alignment	not modelled	96.7	13	PDB header: protein transport Chain: A: PDB Molecule: n-ethylmaleimide sensitive factor; PDBTitle: d2 hexamerization domain of n-ethylmaleimide sensitive factor (nsf)
110	c2dhrC_	Alignment	not modelled	96.7	13	PDB header: hydrolase Chain: C: PDB Molecule: ftsh; PDBTitle: whole cytosolic region of atp-dependent metalloprotease2 ftsh (g399l)
111	c6matE_	Alignment	not modelled	96.6	13	PDB header: ribosomal protein Chain: E: PDB Molecule: rix7 mutant; PDBTitle: cryo-em structure of the essential ribosome assembly aaa-atpase rix7
112	c3m6aC_	Alignment	not modelled	96.6	13	PDB header: hydrolase Chain: C: PDB Molecule: atp-dependent protease la 1; PDBTitle: crystal structure of bacillus subtilis lon c-terminal domain
113	c5mpaL_	Alignment	not modelled	96.6	10	PDB header: hydrolase Chain: L: PDB Molecule: 26s protease subunit rpt4; PDBTitle: 26s proteasome in presence of atp (s2)
114	d1njfa_	Alignment	not modelled	96.6	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
115	c3h4mC_	Alignment	not modelled	96.6	11	PDB header: hydrolase Chain: C: PDB Molecule: proteasome-activating nucleotidase; PDBTitle: aaa atpase domain of the proteasome- activating nucleotidase
116	c1iy2A_	Alignment	not modelled	96.6	15	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent metalloprotease ftsh; PDBTitle: crystal structure of the ftsh atpase domain from thermus2 thermophilus
117	c6em8F_	Alignment	not modelled	96.6	14	PDB header: chaperone Chain: F: PDB Molecule: atp-dependent clp protease atp-binding subunit clpc; PDBTitle: s.aureus clpc resting state, c2 symmetrised
118	d1ny5a2	Alignment	not modelled	96.5	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
119	c4yplE_	Alignment	not modelled	96.5	10	PDB header: hydrolase Chain: E: PDB Molecule: lon protease; PDBTitle: crystal structure of a hexameric lona protease bound to three adps
120	c6hv92_	Alignment	not modelled	96.5	15	PDB header: dna binding protein Chain: 2: PDB Molecule: dna replication licensing factor mcm2; PDBTitle: s. cerevisiae cmg-pol epsilon-dna